

SEQUENCE LISTING

<110> TANABE, TADASHI
YOKOYAMA, CHIEKO

<120> ANTIBODIES SPECIFIC TO HUMAN PROSTACYCLIN SYNTHASE

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<151> 2000-09-27

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<151> 1998-01-10

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<151> 1995-12-28

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<170> PatentIn Ver. 2.1

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 cta tcc cca gcc agg ctg gcc agg cgg gcc cac cgg agc aaa tgg ctg 96
 Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu
 20 25 30
 gag agt tac ctg ctg cac ctg gag gag atg ggt gtg tca gag gag atg 144
 Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met
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Met Ala Trp Ala Ala Leu Leu Gly Leu Leu Ala																	
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Ala Leu Leu Leu Leu Leu Leu Leu Ser Arg Arg Arg Thr Arg Arg Pro																	
15 20 25																	
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Gly Glu Pro Pro Leu Asp Leu Gly Ser Ile Pro Trp Leu Gly Tyr Ala																	
30 35 40																	
ttg gac ttt gga aaa gat gct gcc agc ttc ctc acg agg atg aag gag																	256
Leu Asp Phe Gly Lys Asp Ala Ala Ser Phe Leu Thr Arg Met Lys Glu																	
45 50 55																	
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Lys His Gly Asp Ile Phe Thr Ile Leu Val Gly Gly Arg Tyr Val Thr																	
60 65 70 75																	
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Val Leu Leu Asp Pro His Ser Tyr Asp Ala Val Val Trp Glu Pro Arg																	
80 85 90																	
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Thr Arg Leu Asp Phe His Ala Tyr Ala Ile Phe Leu Met Glu Arg Ile																	
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Phe Asp Val Gln Leu Pro His Tyr Ser Pro Ser Asp Glu Lys Ala Arg																	
110 115 120																	
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Met Lys Leu Thr Leu Leu His Arg Glu Leu Gln Ala Leu Thr Glu Ala																	
125 130 135																	
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Met Tyr Thr Asn Leu His Ala Val Leu Leu Gly Asp Ala Thr Glu Ala																	
140 145 150 155																	
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Gly Ser Gly Trp His Glu Met Gly Leu Leu Asp Phe Ser Tyr Ser Phe																	
160 165 170																	

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Arg	Thr	His	Glu	Ser	Gln	Ala	Gln	Asp	Arg	Val	His	Ser	Ala	Asp	Val	
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Phe	His	Thr	Phe	Arg	Gln	Leu	Asp	Arg	Leu	Leu	Pro	Lys	Leu	Ala	Arg	
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Gly	Ser	Leu	Ser	Val	Gly	Asp	Lys	Asp	His	Met	Cys	Ser	Val	Lys	Ser	
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Arg	Leu															

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His	Ser	Tyr	Asp	Ala	Val	Val	Trp	Glu	Pro	Arg	Thr	Arg	Leu	Asp	Phe	
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His	Ala	Tyr	Ala	Ile	Phe	Leu	Met	Glu	Arg	Ile	Phe	Asp	Val	Gln	Leu	
			100					105					110			
Pro	His	Tyr	Ser	Pro	Ser	Asp	Glu	Lys	Ala	Arg	Met	Lys	Leu	Thr	Leu	
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Leu	His	Arg	Glu	Leu	Gln	Ala	Leu	Thr	Glu	Ala	Met	Tyr	Thr	Asn	Leu	
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Glu	Met	Gly	Leu	Leu	Asp	Phe	Ser	Tyr	Ser	Phe	Leu	Leu	Arg	Ala	Gly	
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Tyr Leu Thr Leu Tyr Gly Ile Glu Ala Leu Pro Arg Thr His Glu Ser
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 Gln Ala Gln Asp Arg Val His Ser Ala Asp Val Phe His Thr Phe Arg
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 Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu
 20 25 30
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 Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met
 35 40 45
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 Gln Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln Gly Asn Met
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 Gly Pro Ala Ala Phe Trp Leu Leu Leu Phe Leu Leu Lys Asn Pro Glu
 65 70 75
 gcc ctg gct gct gtc cgc gga gag ctc gag agt atc ctt tgg caa gcg 287
 Ala Leu Ala Ala Val Arg Gly Glu Leu Glu Ser Ile Leu Trp Gln Ala
 80 85 90 95
 gag cag cct gtc tgc cag acg acc act ctc cca cag aag gtt cta gac 335
 Glu Gln Pro Val Ser Gln Thr Thr Leu Pro Gln Lys Val Leu Asp
 100 105 110
 agc aca cct gtg ctt gat agc gtg ctg agt gag agc ctc agg ctt aca 383
 Ser Thr Pro Val Leu Asp Ser Val Leu Ser Glu Ser Leu Arg Leu Thr
 115 120 125

gct gcc ccc ttc atc acc cgc gag gtt gtg gtg gac ctg gcc atg ccc 431
 Ala Ala Pro Phe Ile Thr Arg Glu Val Val Val Asp Leu Ala Met Pro
 130 135 140

atg gca gac ggg aga gaa ttc aac ctg cga cgt ggt gac cgc ctc ctc 479
 Met Ala Asp Gly Arg Glu Phe Asn Leu Arg Arg Gly Asp Arg Leu Leu
 145 150 155

ctc ttc ccc ttc ctg agc ccc cag aga gac cca gaa atc tac aca gac 527
 Leu Phe Pro Phe Leu Ser Pro Gln Arg Asp Pro Glu Ile Tyr Thr Asp
 160 165 170 175

cca gag gta ttt aaa tac aac cga ttc ctg aac cct gac gga tca gag 575
 Pro Glu Val Phe Lys Tyr Asn Arg Phe Leu Asn Pro Asp Gly Ser Glu
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aag aaa gac ttt tac aag gat ggg aaa cgg ctg aag aat tac aac atg 623
 Lys Lys Asp Phe Tyr Lys Asp Gly Lys Arg Leu Lys Asn Tyr Asn Met
 195 200 205

ccc tgg ggg gcg ggg cac aat cac tgc ctg ggg agg agt tat gcg gtc 671
 Pro Trp Gly Ala Gly His Asn His Cys Leu Gly Arg Ser Tyr Ala Val
 210 215 220

aac agc atc aaa caa ttt gtg ttc ctt gtg ctg gtg cac ttg gac ttg 719
 Asn Ser Ile Lys Gln Phe Val Phe Leu Val Leu Val His Leu Asp Leu
 225 230 235

gag ctg atc aac gca gat gtg gag atc cct gag ttt gac ctc agc agg 767
 Glu Leu Ile Asn Ala Asp Val Glu Ile Pro Glu Phe Asp Leu Ser Arg
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 Tyr Gly Phe Gly Leu Met Gln Pro Glu His Asp Val Pro Val Arg Tyr
 260 265 270

cgc atc cgc cca tgacacaggg agcagatgga tccacgtgct cgcctctgcc 867
 Arg Ile Arg Pro
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Ala	Arg	Ala	Leu	Val	Leu	Gln	Leu	Trp	Ala	Thr	Gln	Gly	Asn	Met	Gly	50	55	60	
Pro	Ala	Ala	Phe	Trp	Leu	Leu	Leu	Phe	Leu	Leu	Lys	Asn	Pro	Glu	Ala	65	70	75	80
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Gln	Pro	Val	Ser	Gln	Thr	Thr	Thr	Leu	Pro	Gln	Lys	Val	Leu	Asp	Ser	100	105	110	
Thr	Pro	Val	Leu	Asp	Ser	Val	Leu	Ser	Glu	Ser	Leu	Arg	Leu	Thr	Ala	115	120	125	
Ala	Pro	Phe	Ile	Thr	Arg	Glu	Val	Val	Val	Asp	Leu	Ala	Met	Pro	Met	130	135	140	
Ala	Asp	Gly	Arg	Glu	Phe	Asn	Leu	Arg	Arg	Gly	Asp	Arg	Leu	Leu	Leu	145	150	155	160
Phe	Pro	Phe	Leu	Ser	Pro	Gln	Arg	Asp	Pro	Glu	Ile	Tyr	Thr	Asp	Pro	165	170	175	
Glu	Val	Phe	Lys	Tyr	Asn	Arg	Phe	Leu	Asn	Pro	Asp	Gly	Ser	Glu	Lys	180	185	190	
Lys	Asp	Phe	Tyr	Lys	Asp	Gly	Lys	Arg	Leu	Lys	Asn	Tyr	Asn	Met	Pro	195	200	205	
Trp	Gly	Ala	Gly	His	Asn	His	Cys	Leu	Gly	Arg	Ser	Tyr	Ala	Val	Asn	210	215	220	
Ser	Ile	Lys	Gln	Phe	Val	Phe	Leu	Val	Leu	Val	His	Leu	Asp	Leu	Glu	225	230	235	240
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Ile Arg Pro
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 Tyr Ala Leu Asp Phe Gly Lys Asp Ala Ala Ser Phe Leu Thr Arg Met
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aag gag aag cac ggt gac atc ttt act ata ctg gtt ggg ggc agg tat 246
 Lys Glu Lys His Gly Asp Ile Phe Thr Ile Leu Val Gly Gly Arg Tyr
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gtc acc gtt ctc ctg gac cca cac tcc tac gac gcg gtg gtg tgg gag 294
 Val Thr Val Leu Leu Asp Pro His Ser Tyr Asp Ala Val Val Trp Glu
 75 80 85

cct cgc acc agg ctc gac ttc cat gcc tat gcc atc ttc ctc atg gag 342
 Pro Arg Thr Arg Leu Asp Phe His Ala Tyr Ala Ile Phe Leu Met Glu
 90 95 100 105

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 Arg Ile Phe Asp Val Gln Leu Pro His Tyr Ser Pro Ser Asp Glu Lys
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 Ala Arg Met Lys Leu Thr Leu Leu His Arg Glu Leu Gln Ala Leu Thr
 125 130 135

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gaa gca ggc agt ggc tgg cac gag atg ggt ctc ctc gac ttc tcc tac	534
Glu Ala Gly Ser Gly Trp His Glu Met Gly Leu Leu Asp Phe Ser Tyr	
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Ser Phe Leu Leu Arg Ala Gly Tyr Leu Thr Leu Tyr Gly Ile Glu Ala	
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Asp Val Phe His Thr Phe Arg Gln Leu Asp Arg Leu Leu Pro Lys Leu	
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Lys Ser Arg Leu Trp Lys Leu Leu Ser Pro Ala Arg Leu Ala Arg Arg	
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Ala His Arg Ser Lys Trp Leu Glu Ser Tyr Leu Leu His Leu Glu Glu	
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Val Val Asp Leu Ala Met Pro Met Ala Asp Gly Arg Glu Phe Asn Leu	
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 380 385 390

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 Asp Pro Glu Ile Tyr Thr Asp Pro Glu Val Phe Lys Tyr Asn Arg Phe
 395 400 405

ctg aac cct gac gga tca gag aag aaa gac ttt tac aag gat ggg aaa 1302
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 410 415 420 425

cgg ctg aag aat tac aac atg ccc tgg ggg gcg ggg cac aat cac tgc 1350
 Arg Leu Lys Asn Tyr Asn Met Pro Trp Gly Ala Gly His Asn His Cys
 430 435 440

ctg ggg agg agt tat gcg gtc aac agc atc aaa caa ttt gtg ttc ctt 1398
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 445 450 455

gtg ctg gtg cac ttg gac ttg gag ctg atc aac gca gat gtg gag atc 1446
 Val Leu Val His Leu Asp Leu Glu Leu Ile Asn Ala Asp Val Glu Ile
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 Pro Glu Phe Asp Leu Ser Arg Tyr Gly Phe Gly Leu Met Gln Pro Glu
 475 480 485

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 His Asp Val Pro Val Arg Tyr Arg Ile Arg Pro
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gctgggtcca ggggagggaa aagctaagag ggtgaacaaa gaaaagacat tgaaagctct 1727

atggattatc cactgcaaag ttttctttcc aaaatcaggc tttgtctgct cccaattcac 1787

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<213> Homo sapiens

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5

10

15

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 65 70 75 80
 His Ser Tyr Asp Ala Val Val Trp Glu Pro Arg Thr Arg Leu Asp Phe
 85 90 95
 His Ala Tyr Ala Ile Phe Leu Met Glu Arg Ile Phe Asp Val Gln Leu
 100 105 110
 Pro His Tyr Ser Pro Ser Asp Glu Lys Ala Arg Met Lys Leu Thr Leu
 115 120 125
 Leu His Arg Glu Leu Gln Ala Leu Thr Glu Ala Met Tyr Thr Asn Leu
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 195 200 205
 Gln Leu Asp Arg Leu Leu Pro Lys Leu Ala Arg Gly Ser Leu Ser Val
 210 215 220
 Gly Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu
 225 230 235 240
 Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu
 245 250 255
 Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met
 260 265 270
 Gln Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln Gly Asn Met
 275 280 285
 Gly Pro Ala Ala Phe Trp Leu Leu Leu Phe Leu Leu Lys Asn Pro Glu
 290 295 300
 Ala Leu Ala Ala Val Arg Gly Glu Leu Glu Ser Ile Leu Trp Gln Ala
 305 310 315 320

Glu	Gln	Pro	Val	Ser	Gln	Thr	Thr	Thr	Leu	Pro	Gln	Lys	Val	Leu	Asp	
				325					330					335		
Ser	Thr	Pro	Val	Leu	Asp	Ser	Val	Leu	Ser	Glu	Ser	Leu	Arg	Leu	Thr	
				340					345					350		
Ala	Ala	Pro	Phe	Ile	Thr	Arg	Glu	Val	Val	Val	Asp	Leu	Ala	Met	Pro	
				355					360					365		
Met	Ala	Asp	Gly	Arg	Glu	Phe	Asn	Leu	Arg	Arg	Gly	Asp	Arg	Leu	Leu	
				370					375					380		
Leu	Phe	Pro	Phe	Leu	Ser	Pro	Gln	Arg	Asp	Pro	Glu	Ile	Tyr	Thr	Asp	
				385					390					395		
Pro	Glu	Val	Phe	Lys	Tyr	Asn	Arg	Phe	Leu	Asn	Pro	Asp	Gly	Ser	Glu	
				405					410					415		
Lys	Lys	Asp	Phe	Tyr	Lys	Asp	Gly	Lys	Arg	Leu	Lys	Asn	Tyr	Asn	Met	
				420					425					430		
Pro	Trp	Gly	Ala	Gly	His	Asn	His	Cys	Leu	Gly	Arg	Ser	Tyr	Ala	Val	
				435					440					445		
Asn	Ser	Ile	Lys	Gln	Phe	Val	Phe	Leu	Val	Leu	Val	His	Leu	Asp	Leu	
				450					455					460		
Glu	Leu	Ile	Asn	Ala	Asp	Val	Glu	Ile	Pro	Glu	Phe	Asp	Leu	Ser	Arg	
				465					470					475		
Tyr	Gly	Phe	Gly	Leu	Met	Gln	Pro	Glu	His	Asp	Val	Pro	Val	Arg	Tyr	
				485					490					495		
Arg	Ile	Arg	Pro													
				500												

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24

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<220>
<223> Description of Artificial Sequence: Synthetic
peptide

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Gly Val Glu Ala Pro Pro His Thr Gln Glu Ser Gln
1 5 10

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<212> PRT
<213> Artificial Sequence

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1 5 10